



SUBSTITUTE SEQUENCE LISTING

<110> Cahoon, Rebecca E.  
Miao, Guo-Hua  
Herrman, Rafael  
Rafalski, Antoni  
McCutchen, Bill F.

<120> Plant Protein Disulfide Isomerases

<130> BB1085 US NA

<140> 09/417,251

<141> 1999-10-13

<150> 60/049,408

<151> 1998-10-15

<160> 20

<170> Microsoft Office 97

<210> 1

<211> 504

<212> DNA

<213> Zea mays

<220>

<221> unsure

<222> (463)

<223> n is a, c, g or t

<220>

<221> unsure

<222> (469)

<223> n is a, c, g or t

<220>

<221> unsure

<222> (471)

<223> n is a, c, g or t

<220>

<221> unsure

<222> (496)

<223> n is a, c, g or t

<400> 1

tgctgcccct gtctgtctct gttcagcgga accttctctt tgtgttttat aggttacccc 60  
gtcaaaaaga cagcccatca tgcaccacaa gaagatcgcc tgcagcttca tggctgctct 120  
ggctgacctat gcctctgctg ccgactcaga tgttcacacag ctaaccaagg acaccttcga 180  
ggagtttgctc aagtccaaca atctcgctct cgctgagttc tttgctccct ggtgcgggtca 240  
ctgcaaggcc ctcgcccccg agtacgagga ggccgccaca actctcaagg agaagaacat 300  
caagcttgcc aagattgact gcaactgagga gtccgacctc tgcaaagacc agggcgctga 360  
gggttacccc accctcaagg tcttcctgtg tcttgacaat gtcactccct actctggcca 420  
gcgtaaggcc gctggtatca ttctacatga ttaagagttc ctnccecgng nttcatttta 480  
caaagggaac cctcgnnggt ttaa 504

<210> 2

<211> 110

RECEIVED

JUN 18 2004

TECH CENTER 1600/2900

<212> PRT  
<213> Zea mays

<400> 2  
Met Ala Ala Leu Ala Ala Tyr Ala Ser Ala Ala Asp Ser Asp Val His  
1 5 10 15  
Gln Leu Thr Lys Asp Thr Phe Glu Glu Phe Val Lys Ser Asn Asn Leu  
20 25 30  
Val Leu Ala Glu Phe Phe Ala Pro Trp Cys Gly His Cys Lys Ala Leu  
35 40 45  
Ala Pro Glu Tyr Glu Glu Ala Ala Thr Thr Leu Lys Glu Lys Asn Ile  
50 55 60  
Lys Leu Ala Lys Ile Asp Cys Thr Glu Glu Ser Asp Leu Cys Lys Asp  
65 70 75 80  
Gln Gly Val Glu Gly Tyr Pro Thr Leu Lys Val Phe Arg Gly Leu Asp  
85 90 95  
Asn Val Thr Pro Tyr Ser Gly Gln Arg Lys Ala Ala Gly Ile  
100 105 110

<210> 3  
<211> 505  
<212> DNA  
<213> Glycine max

<220>  
<221> unsure  
<222> (503)  
<223> n is a, c, g or t

<400> 3  
tctttctggt actccacctg gtattgttgt tgaagatcgt aataccaata aaaattatgt 60  
ttatccacaa gctaataaaa ttactgaaga tgcattacgt gcacatttac aagggttatgt 120  
tgatggtaca ctccaacca ctgtcaaata tgaagaaatc ccagaaaaac aagatgggtcc 180  
agtttatgta ctctggtggtg aaaattttga atccattgtt atggatgaaa cttaaagatgt 240  
attagttgaä ttttatgcac catggtgtgg acattgtaaa acattagctc ccaaatacga 300  
tgcattaggt gaatcattca agtcaaacc ccaatgtcatt attgccaaga ttgatgccac 360  
tgcaaatgat acccctgttg atattcaagg tttcccccact attatctatt ggccagctaa 420  
taataagaaa aatccaatta catatgaagg tgaacgtact gaatcagcac ttgctgcatt 480  
tgtacgtgaa aaatggtcaa cantt 505

<210> 4  
<211> 158  
<212> PRT  
<213> Glycine max

<400> 4  
Pro Gly Ile Val Val Glu Asp Arg Asn Thr Asn Lys Asn Tyr Val Tyr  
1 5 10 15  
Pro Gln Ala Asn Glu Ile Thr Glu Asp Ala Leu Arg Ala His Leu Gln  
20 25 30  
Gly Tyr Val Asp Gly Thr Leu Gln Pro Thr Val Lys Ser Glu Glu Ile  
35 40 45

Pro Glu Lys Gln Asp Gly Pro Val Tyr Val Leu Val Gly Lys Asn Phe  
 50 55 60

Glu Ser Ile Val Met Asp Glu Thr Lys Asp Val Leu Val Glu Phe Tyr  
 65 70 75 80

Ala Pro Trp Cys Gly His Cys Lys Thr Leu Ala Pro Lys Tyr Asp Ala  
 85 90 95

Leu Gly Glu Ser Phe Lys Ser Asn Pro Asn Val Ile Ile Ala Lys Ile  
 100 105 110

Asp Ala Thr Ala Asn Asp Thr Pro Val Asp Ile Gln Gly Phe Pro Thr  
 115 120 125

Ile Ile Tyr Trp Pro Ala Asn Asn Lys Lys Asn Pro Ile Thr Tyr Glu  
 130 135 140

Gly Glu Arg Thr Glu Ser Ala Leu Ala Ala Phe Val Arg Glu  
 145 150 155

<210> 5  
 <211> 1692  
 <212> DNA  
 <213> Zea mays

<400> 5  
 gcacgaggcg cggcggagat cgaatcgagc gcccgccacg gcgatggcga ctagagtcct 60  
 gccgceggct ctgctctctt tcatactcct cctgctgctc tcgctctcag cccgcgacac 120  
 cgtcgccgcg ggcgaggatt tccccgcgga cgggcggggtg atcgacctcg acgacagcaa 180  
 tttcgaggcg gcgctgggag ccategactt tctcttcgtc gacttctacg ccccttggtg 240  
 cggccactgc aagagacttg cggccgagtt agatgaagct gcaccgggtg tgtcagggtt 300  
 gagtgagcct attgtgtgtg ccaaagtcaa cgctgataaa tacagaaaac tcggatcaaa 360  
 atatggagtg gatgggttcc ctacctcoat gctctttatc catgggtgtt caattgaata 420  
 cactggttcg aggaaagctg accagcttgt ccgcaatctg aagaagttcg tttcgccaga 480  
 tgtttctatc cttgagtcag attctgcgat aaagaacttt gttgagaatg ctgggataag 540  
 ctttccgata ttccttggtt ttggggtgaa tgactcattg attgctgagt atggaaggaa 600  
 atacaagaaa agagcctggt ttgctgttgc taaagatttc tctgaggaca tcatggtagc 660  
 ctatgaattt gataaggttc cagcactagt tgctatccat ccaaagtata aggaacagag 720  
 tttgttctat ggcccatttg aagaaaattt cttagaagat tttgtacggc aatcccttct 780  
 ccctttgggt gtcccaatca atacagagac actaaaaatg ctgaatgatg atcagaggaa 840  
 agttgttctc acaattttgg aggatgattc agatgaaaac tctacgcaac tggtaaagat 900  
 tttgcgatct gctgctaattg caaacctgta tttgggtgtt ggatatgttg gaatcaagca 960  
 atgggatggg tttgtggaga cttttgatgt ttccaagagc tcacagctgc caaagctact 1020  
 tgttgtggat agagatgagg agtatgagct agtggatggt tcagagagat tagaagaagg 1080  
 tgaccaagca tctcaaataa gccaatcctt tgagggatag agagcaggaa gaacaacaaa 1140  
 gaagaaaatc accggccctt ctttcatggg tttcctgaac tctctggtca gcctgaactc 1200  
 gctgtacatc cttatatttg tcatcgccct tctgtttgtc atggtgtact ttgctgggca 1260  
 agatgatact cctcagccaa gacgaattca cgaagagtga tgaaagcttg ttgggcttct 1320  
 tgcacctaaa gatggctaatt ctaccgggag attagctttt gtattaattg tacaaaagct 1380  
 tcaactgacg caagtctgta agagtgggtt tggcaatttg gccattcatg ctgagtttct 1440  
 tcaatctcta ttggcgacat caatttctgc atcctgccta tttgtgttct tgctttgtgc 1500  
 ctttcaattt gttctttaat ttagagctta gaaattagcc tctgcctgtg tattctggaa 1560  
 cctgccattc cagagtcctt ttctgtgaaa atatatttat tattatcata ctctgctacc 1620  
 gagcttttgt acaattaata caggatatat agactgttct ggtgcacaaa aaaaaaaga 1680  
 aaaaaaaaaa aa 1692

<210> 6  
 <211> 418

<212> PRT  
<213> Zea mays

<400> 6

Met Ala Thr Arg Val Leu Pro Pro Ala Leu Leu Ser Phe Ile Leu Leu  
1 5 10 15  
Leu Leu Leu Ser Leu Ser Ala Arg Asp Thr Val Ala Ala Gly Glu Asp  
20 25 30  
Phe Pro Arg Asp Gly Arg Val Ile Asp Leu Asp Asp Ser Asn Phe Glu  
35 40 45  
Ala Ala Leu Gly Ala Ile Asp Phe Leu Phe Val Asp Phe Tyr Ala Pro  
50 55 60  
Trp Cys Gly His Cys Lys Arg Leu Ala Pro Glu Leu Asp Glu Ala Ala  
65 70 75 80  
Pro Val Leu Ser Gly Leu Ser Glu Pro Ile Val Val Ala Lys Val Asn  
85 90 95  
Ala Asp Lys Tyr Arg Lys Leu Gly Ser Lys Tyr Gly Val Asp Gly Phe  
100 105 110  
Pro Thr Leu Met Leu Phe Ile His Gly Val Pro Ile Glu Tyr Thr Gly  
115 120 125  
Ser Arg Lys Ala Asp Gln Leu Val Arg Asn Leu Lys Lys Phe Val Ser  
130 135 140  
Pro Asp Val Ser Ile Leu Glu Ser Asp Ser Ala Ile Lys Asn Phe Val  
145 150 155 160  
Glu Asn Ala Gly Ile Ser Phe Pro Ile Phe Leu Gly Phe Gly Val Asn  
165 170 175  
Asp Ser Leu Ile Ala Glu Tyr Gly Arg Lys Tyr Lys Lys Arg Ala Trp  
180 185 190  
Phe Ala Val Ala Lys Asp Phe Ser Glu Asp Ile Met Val Ala Tyr Glu  
195 200 205  
Phe Asp Lys Val Pro Ala Leu Val Ala Ile His Pro Lys Tyr Lys Glu  
210 215 220  
Gln Ser Leu Phe Tyr Gly Pro Phe Glu Glu Asn Phe Leu Glu Asp Phe  
225 230 235 240  
Val Arg Gln Ser Leu Leu Pro Leu Val Val Pro Ile Asn Thr Glu Thr  
245 250 255  
Leu Lys Met Leu Asn Asp Asp Gln Arg Lys Val Val Leu Thr Ile Leu  
260 265 270  
Glu Asp Asp Ser Asp Glu Asn Ser Thr Gln Leu Val Lys Ile Leu Arg  
275 280 285  
Ser Ala Ala Asn Ala Asn Arg Asp Leu Val Phe Gly Tyr Val Gly Ile  
290 295 300

Lys Gln Trp Asp Gly Phe Val Glu Thr Phe Asp Val Ser Lys Ser Ser  
 305 310 315 320  
 Gln Leu Pro Lys Leu Leu Val Trp Asp Arg Asp Glu Glu Tyr Glu Leu  
 325 330 335  
 Val Asp Gly Ser Glu Arg Leu Glu Glu Gly Asp Gln Ala Ser Gln Ile  
 340 345 350  
 Ser Gln Phe Leu Glu Gly Tyr Arg Ala Gly Arg Thr Thr Lys Lys Lys  
 355 360 365  
 Ile Thr Gly Pro Ser Phe Met Gly Phe Leu Asn Ser Leu Val Ser Leu  
 370 375 380  
 Asn Ser Leu Tyr Ile Leu Ile Phe Val Ile Ala Leu Leu Phe Val Met  
 385 390 395 400  
 Val Tyr Phe Ala Gly Gln Asp Asp Thr Pro Gln Pro Arg Arg Ile His  
 405 410 415

Glu Glu

<210> 7  
 <211> 1774  
 <212> DNA  
 <213> Momordica charantia

<400> 7  
 gcacgaggag ccggatgcgg cggccgggtgc ttccgctcat cgtcacctcc ccgactttga 60  
 tggttttgag ggaggtgccg aggacgagga ttttggggac ttctccgatt ttgaggactc 120  
 ggatgctgat cgggatgagt acaaggcgcc ggaggtggac gagaaggatg tcgtcgtgtt 180  
 gaaggagggt aacttcagcg atttcgtgga gaagaaccgg tttgttatgg tggagtttta 240  
 cgctccctgg tgtggtcact gccaggcgct ggccggcgag tatgctgctg ccgccactga 300  
 attgaaaggc gagaacgtgg ttttggcgaa ggttgatgcg acggaggaga atgaattgtc 360  
 gcagaagtac gacgttcaag gatttccgac tgtttatttc tttgccgatg gagtccacaa 420  
 gtcttaccct ggacagcgga ccaaggatgc tatagtaacc tggatcaaga agaagatcgg 480  
 acctggtatt tacaacataa cttcgggtgga agatgctgaa cgcatactga cttctgagac 540  
 taaagttggt cttggttacc tgaactcctt ggtgggcccct gagagcaatg agcttgctgc 600  
 tgcttcaaga ctggaagatg atgtcaactt ttaccaaacg gtggatcctg aagtggccaa 660  
 gctttttccac attgaagctt cagcaaaaacg ccctgccttg gtattgctta agaaggaggc 720  
 tgaaaaactg aaccgctttg atggcgagtt ttctaagtct gcaattgctg aatttggtt 780  
 tgccaataag cttccattag ttacaaagt ttacgagagaa agcgcaccat tgattttcga 840  
 aagttcaatt aagaaacagt tgattctatt tgcgatttca aatgattcag agaaactaat 900  
 ccccatatth gaagagtcgt cgaagtcttt taaaggaaag cttatttttcg tttatgtgga 960  
 aattgacaat gaagatgttg gaaagccggt atcagaatac tttggcatta gtggcaatgg 1020  
 tccagaggtt cttggataca ctggaaatga ggacagcaag aaatttggtc ttgctaagga 1080  
 agttactttg gataatatta aggttttcgg agaaaatttc ttggaagaca agttaaacc 1140  
 cttttataag tcagatccca ttcctgagac taatgatggt gacgtgaaag tagtggttg 1200  
 agacaacttc gacaatattg ttttagatga atcgaaggat gttctcctcg agatctatgc 1260  
 tccttggtgt gggcattgcc aagcactgga accaacttat aacaagcttg ccaaactatt 1320  
 acgtggcatc gattcacttg tcattgctaa gatggatggc acaacaaatg aacatccccg 1380  
 ggcaagtc gatggattcc caacaattct gtttttccca gctggaaaca agagctttga 1440  
 ccctatcact gtcgataccg atcgtaccgt tgtggcactg tacaaattca tcaagaaaaa 1500  
 tgcattccatc cttttcaagc tacagaagcc agtttcgagt ccgaaagccg taagttctga 1560  
 agccaaatct ggtgatgcca aagagagccc aaagagcagc accactgacg taaaggatga 1620  
 attgtgaaga cttcttaaat agttttgtaa gttattatcc catcttttat gcactttttg 1680  
 cagctgccag attttttagac catatggaga gactagaaat taaaagaaaa tgtttttttc 1740

ccttttttctt taggaaaaaa aaaaaaaaaa aaaa

1774

<210> 8

<211> 541

<212> PRT

<213> Momordica charantia

<400> 8

His Glu Glu Pro Asp Ala Ala Ala Gly Ala Ser Ala His Arg His Leu  
1 5 10 15

Pro Asp Phe Asp Gly Phe Glu Gly Gly Ala Glu Asp Glu Asp Phe Gly  
20 25 30

Asp Phe Ser Asp Phe Glu Asp Ser Asp Ala Asp Arg Asp Glu Tyr Lys  
35 40 45

Ala Pro Glu Val Asp Glu Lys Asp Val Val Val Leu Lys Glu Gly Asn  
50 55 60

Phe Ser Asp Phe Val Glu Lys Asn Arg Phe Val Met Val Glu Phe Tyr  
65 70 75 80

Ala Pro Trp Cys Gly His Cys Gln Ala Leu Ala Pro Glu Tyr Ala Ala  
85 90 95

Ala Ala Thr Glu Leu Lys Gly Glu Asn Val Val Leu Ala Lys Val Asp  
100 105 110

Ala Thr Glu Glu Asn Glu Leu Ser Gln Lys Tyr Asp Val Gln Gly Phe  
115 120 125

Pro Thr Val Tyr Phe Phe Ala Asp Gly Val His Lys Ser Tyr Pro Gly  
130 135 140

Gln Arg Thr Lys Asp Ala Ile Val Thr Trp Ile Lys Lys Lys Ile Gly  
145 150 155 160

Pro Gly Ile Tyr Asn Ile Thr Ser Val Glu Asp Ala Glu Arg Ile Leu  
165 170 175

Thr Ser Glu Thr Lys Val Val Leu Gly Tyr Leu Asn Ser Leu Val Gly  
180 185 190

Pro Glu Ser Asn Glu Leu Ala Ala Ala Ser Arg Leu Glu Asp Asp Val  
195 200 205

Asn Phe Tyr Gln Thr Val Asp Pro Glu Val Ala Lys Leu Phe His Ile  
210 215 220

Glu Ala Ser Ala Lys Arg Pro Ala Leu Val Leu Leu Lys Lys Glu Ala  
225 230 235 240

Glu Lys Leu Asn Arg Phe Asp Gly Glu Phe Ser Lys Ser Ala Ile Ala  
245 250 255

Glu Phe Val Phe Ala Asn Lys Leu Pro Leu Val Thr Lys Phe Thr Arg  
260 265 270

Glu Ser Ala Pro Leu Ile Phe Glu Ser Ser Ile Lys Lys Gln Leu Ile  
 275 280 285  
 Leu Phe Ala Ile Ser Asn Asp Ser Glu Lys Leu Ile Pro Ile Phe Glu  
 290 295 300  
 Glu Ser Ser Lys Ser Phe Lys Gly Lys Leu Ile Phe Val Tyr Val Glu  
 305 310 315 320  
 Ile Asp Asn Glu Asp Val Gly Lys Pro Val Ser Glu Tyr Phe Gly Ile  
 325 330 335  
 Ser Gly Asn Gly Pro Glu Val Leu Gly Tyr Thr Gly Asn Glu Asp Ser  
 340 345 350  
 Lys Lys Phe Val Leu Ala Lys Glu Val Thr Leu Asp Asn Ile Lys Ala  
 355 360 365  
 Phe Gly Glu Asn Phe Leu Glu Asp Lys Leu Lys Pro Phe Tyr Lys Ser  
 370 375 380  
 Asp Pro Ile Pro Glu Thr Asn Asp Gly Asp Val Lys Val Val Val Gly  
 385 390 395 400  
 Asp Asn Phe Asp Asn Ile Val Leu Asp Glu Ser Lys Asp Val Leu Leu  
 405 410 415  
 Glu Ile Tyr Ala Pro Trp Cys Gly His Cys Gln Ala Leu Glu Pro Thr  
 420 425 430  
 Tyr Asn Lys Leu Ala Lys His Leu Arg Gly Ile Asp Ser Leu Val Ile  
 435 440 445  
 Ala Lys Met Asp Gly Thr Thr Asn Glu His Pro Arg Ala Lys Ser Asp  
 450 455 460  
 Gly Phe Pro Thr Ile Leu Phe Phe Pro Ala Gly Asn Lys Ser Phe Asp  
 465 470 475 480  
 Pro Ile Thr Val Asp Thr Asp Arg Thr Val Val Ala Leu Tyr Lys Phe  
 485 490 495  
 Ile Lys Lys Asn Ala Ser Ile Pro Phe Lys Leu Gln Lys Pro Val Ser  
 500 505 510  
 Ser Pro Lys Ala Val Ser Ser Glu Ala Lys Ser Gly Asp Ala Lys Glu  
 515 520 525  
 Ser Pro Lys Ser Ser Thr Thr Asp Val Lys Asp Glu Leu  
 530 535 540

<210> 9  
 <211> 2031  
 <212> DNA  
 <213> Zea mays

<400> 9  
 ctcaccagct gcccgcgcat ccaattcctc tcgctggacg gctgcagcac atcatcaggt 60  
 gagaccgtga gagggatgg gatcaacaac aatgtcccct ccatcttttc ccgtcgtcct 120  
 cctgctcctc ctccctcgcca ccatagccgc agccgcccga agcaacatgg atgaggaggt 180

```

ggtggacgac ctccagtatc ttattgacaa ctccgacgac atccccacca acgatcccg 240
cgggtggcct gagggagact acgacgacga cgaccttctc ttccaagatc aggaccagga 300
cctcacaggc caccagccgg agatcgacga gacccacgta gtggtcctcg ccgccgcaaa 360
cttttctctc ttctctgcct ccagccacca tggtatggtt gagttctacg caccttggtg 420
tgggcactgc caggagctcg ccccgggatt aagccggcgc cgcgcgcac tcgccggctc 480
aaccaacca ccaaggccca acttcgccct tgccaaggct gacgccaccg aggaaaccga 540
cctcgcccag aagtacgacg tccagggtt cccaccatc ctcttcttca tcgatggcgt 600
ccccagaggc tataacggag ccaggacca ggaagccatc gtcgactgga tcaacaagaa 660
gctcggccca gccgtgcaaa atgtcaccag cgtcgacgag gccagagca tactcaccgg 720
agatgacaaa gccgtccttg ccttctctga cacactatcc ggtgctcaca gtgatgagct 780
tgctgtgct tcgaggctgg aagatagcat caacttttat cagacttcga ctctgtgct 840
tgctaagctt ttccatatcg atgcagcgc gaagcgtcca tccgtagtgc tgctgaagaa 900
agaggaggag aagttgacct tctatgatgg ggagtttaaa gcatcagcca ttgctggtt 960
tgtgtctgct aacaagcttc ctttggtgac cacactaact caagaaactt ccccttctat 1020
ttttggcaat ccaatcaaga agcagatttt actatttgct gttgcaagcg agtccacca 1080
atctctgccc atctttaagg aagcagcaaa accatttaag ggaaagtat tatttgtctt 1140
tgtggaacga gacagtgagg aagttggtga accagttgcc gactactttg gtattactgg 1200
acaagagacc acagttcttg cttacactgg taatgaagat gctaggaaat ttttcttga 1260
tggtgaggtg tcaactgaag ctataaagga cttcgctgaa ggtttcttg aagacaagct 1320
tacaccattc tacaatcgg aaccagtgc tgaatcta atgatgggat tgaaaattgt 1380
tggtgggaag aatctggatc taatagttt tgatgaaaca aaagatgtac ttcttgagat 1440
atatgcacca tgggtgggtc attgtcaatc gctggaacct acttacaaca atctagccaa 1500
gcatctacgt agtgttgact cccttggtg agccaaaatg gatggtacta ccaatgagca 1560
tccacgtgca aagtctgacg gataccgcg gattctcttc tatccagctg ggaagaaaag 1620
ctttgagcca atcacttttg agggggagcg gacagtggta gatctgtaca agttcatcaa 1680
gaaacatgct agcatccctt tcaagttgaa gcgccaggag tcgagaaccg agagcactg 1740
ggcggagggt gtgaagagct ctggtacgaa ctcaaaggac gaactgtaaa gagctcaggg 1800
ttggatgtgt gttggagtgg atcaggggtga aagtttccat ctcaatacaa gtagatcgat 1860
cttggtggat gcgagtgacg tgttggcctg agggaggagc agcagagatg agtgcttact 1920
gcttagagag aggaatgaaa tcagcaacta atcaaataaa atcaaattcc attaaaaaaa 1980
aaaaaaaaa taaaaaaaaa aaaattaaaa aaaaataaaa aaaaaaaaaa a 2031

```

<210> 10  
 <211> 570  
 <212> PRT  
 <213> Zea mays

<400> 10  
 Met Gly Ser Thr Thr Met Ser Pro Pro Ser Phe Pro Val Val Leu Leu  
 1 5 10 15  
 Leu Leu Leu Leu Ala Thr Ile Ala Ala Ala Ala Gly Ser Asn Met Asp  
 20 25 30  
 Glu Glu Val Val Asp Asp Leu Gln Tyr Leu Ile Asp Asn Ser Asp Asp  
 35 40 45  
 Ile Pro Thr Asn Asp Pro Asp Gly Trp Pro Glu Gly Asp Tyr Asp Asp  
 50 55 60  
 Asp Asp Leu Leu Phe Gln Asp Gln Asp Gln Asp Leu Thr Gly His Gln  
 65 70 75 80  
 Pro Glu Ile Asp Glu Thr His Val Val Val Leu Ala Ala Ala Asn Phe  
 85 90 95  
 Ser Ser Phe Leu Ala Ser Ser His His Val Met Val Glu Phe Tyr Ala  
 100 105 110



Pro Trp Cys Gly His Cys Gln Glu Leu Ala Pro Gly Leu Ser Arg Arg  
 115 120 125  
 Arg Ala His Leu Ala Gly Ser Thr Asn Gln Pro Arg Pro Asn Phe Ala  
 130 135 140  
 Leu Ala Lys Val Asp Ala Thr Glu Glu Thr Asp Leu Ala Gln Lys Tyr  
 145 150 155 160  
 Asp Val Gln Gly Phe Pro Thr Ile Leu Phe Phe Ile Asp Gly Val Pro  
 165 170 175  
 Arg Gly Tyr Asn Gly Ala Arg Thr Lys Glu Ala Ile Val Asp Trp Ile  
 180 185 190  
 Asn Lys Lys Leu Gly Pro Ala Val Gln Asn Val Thr Ser Val Asp Glu  
 195 200 205  
 Ala Gln Ser Ile Leu Thr Gly Asp Asp Lys Ala Val Leu Ala Phe Leu  
 210 215 220  
 Asp Thr Leu Ser Gly Ala His Ser Asp Glu Leu Ala Ala Ala Ser Arg  
 225 230 235 240  
 Leu Glu Asp Ser Ile Asn Phe Tyr Gln Thr Ser Thr Pro Asp Val Ala  
 245 250 255  
 Lys Leu Phe His Ile Asp Ala Ala Ala Lys Arg Pro Ser Val Val Leu  
 260 265 270  
 Leu Lys Lys Glu Glu Glu Lys Leu Thr Phe Tyr Asp Gly Glu Phe Lys  
 275 280 285  
 Ala Ser Ala Ile Ala Gly Phe Val Ser Ala Asn Lys Leu Pro Leu Val  
 290 295 300  
 Thr Thr Leu Thr Gln Glu Thr Ser Pro Ser Ile Phe Gly Asn Pro Ile  
 305 310 315 320  
 Lys Lys Gln Ile Leu Leu Phe Ala Val Ala Ser Glu Ser Thr Lys Phe  
 325 330 335  
 Leu Pro Ile Phe Lys Glu Ala Ala Lys Pro Phe Lys Gly Lys Leu Leu  
 340 345 350  
 Phe Val Phe Val Glu Arg Asp Ser Glu Glu Val Gly Glu Pro Val Ala  
 355 360 365  
 Asp Tyr Phe Gly Ile Thr Gly Gln Glu Thr Thr Val Leu Ala Tyr Thr  
 370 375 380  
 Gly Asn Glu Asp Ala Arg Lys Phe Phe Leu Asp Gly Glu Val Ser Leu  
 385 390 395 400  
 Glu Ala Ile Lys Asp Phe Ala Glu Gly Phe Leu Glu Asp Lys Leu Thr  
 405 410 415  
 Pro Phe Tyr Lys Ser Glu Pro Val Pro Glu Ser Asn Asp Gly Asp Val  
 420 425 430

Lys Ile Val Val Gly Lys Asn Leu Asp Leu Ile Val Phe Asp Glu Thr  
 435 440 445  
 Lys Asp Val Leu Leu Glu Ile Tyr Ala Pro Trp Cys Gly His Cys Gln  
 450 455 460  
 Ser Leu Glu Pro Thr Tyr Asn Asn Leu Ala Lys His Leu Arg Ser Val  
 465 470 475 480  
 Asp Ser Leu Val Val Ala Lys Met Asp Gly Thr Thr Asn Glu His Pro  
 485 490 495  
 Arg Ala Lys Ser Asp Gly Tyr Pro Thr Ile Leu Phe Tyr Pro Ala Gly  
 500 505 510  
 Lys Lys Ser Phe Glu Pro Ile Thr Phe Glu Gly Glu Arg Thr Val Val  
 515 520 525  
 Asp Leu Tyr Lys Phe Ile Lys Lys His Ala Ser Ile Pro Phe Lys Leu  
 530 535 540  
 Lys Arg Gln Glu Ser Arg Thr Glu Ser Thr Arg Ala Glu Gly Val Lys  
 545 550 555 560  
 Ser Ser Gly Thr Asn Ser Lys Asp Glu Leu  
 565 570

<210> 11  
 <211> 891  
 <212> DNA  
 <213> Zea mays

<400> 11  
 gcacgagtgg aaatggataa cgaagatggt ggaaagcctg tttcagaata ctttggtatc 60  
 agtgggaatg ctccaaaagt acttggatac actgggaatg atgatggaaa aaaatttgtg 120  
 cttgatggag aggtgactac tgacaaaatt aaggcatttg gggaagattt cgttgaagac 180  
 aagctaaaac cttttttacaa gtcagatcca gtccctgaaa gtaatgatgg tgatgtgaaa 240  
 atagtagttg gtaataattt tgatgaaatt gtcttgatg agtcaaagga tgttctcctc 300  
 gagatttatg tcacctgggtg tggccattgc caatcactgg agccaatata caacaagctt 360  
 gcaaaacatc ttgcgaatat tgattctctt gtaatagcca agatggatgg aacaacaaat 420  
 gagcatccca gggctaagcc tgatggattc cccactcttc tcttcttccc ggcaggaaac 480  
 aagagttttg accctattac tgttgatata gatcgtagag tggtagcctt ctacaagtgc 540  
 ctcaagaaac atgcatcaat cccattcaag ctccagaaac caacctcaac ttctgaatcc 600  
 gattccaagg ggagctctga tgccaaagag agccagagta gtgatgtgaa ggacgaatta 660  
 tgaggagtta agtgatatat ttttatttat agaaactatg attcagacag atgatgacat 720  
 agtgactgag gtaaaaaata ccaagttact tctcaccctt ggtcaataaa aaacaaacgg 780  
 ggagtggggg gagagagaca aatgcgaggc acacatgtat tactattaac ttcaatttgt 840  
 acaacagtgg gtaatttaga attttgattt tgggttgaga cttcaaaaaa a 891

<210> 12  
 <211> 220  
 <212> PRT  
 <213> Zea mays

<400> 12  
 Ala Arg Val Glu Met Asp Asn Glu Asp Val Gly Lys Pro Val Ser Glu  
 1 5 10 15  
 Tyr Phe Gly Ile Ser Gly Asn Ala Pro Lys Val Leu Gly Tyr Thr Gly  
 20 25 30

Asn Asp Asp Gly Lys Lys Phe Val Leu Asp Gly Glu Val Thr Thr Asp  
                   35                                  40                                  45  
 Lys Ile Lys Ala Phe Gly Glu Asp Phe Val Glu Asp Lys Leu Lys Pro  
           50                                  55                                  60  
 Phe Tyr Lys Ser Asp Pro Val Pro Glu Ser Asn Asp Gly Asp Val Lys  
           65                                  70                                  75                                  80  
 Ile Val Val Gly Asn Asn Phe Asp Glu Ile Val Leu Asp Glu Ser Lys  
                                   85                                  90                                  95  
 Asp Val Leu Leu Glu Ile Tyr Ala Pro Trp Cys Gly His Cys Gln Ser  
                                   100                                  105                                  110  
 Leu Glu Pro Ile Tyr Asn Lys Leu Ala Lys His Leu Arg Asn Ile Asp  
                                   115                                  120                                  125  
 Ser Leu Val Ile Ala Lys Met Asp Gly Thr Thr Asn Glu His Pro Arg  
           130                                  135                                  140  
 Ala Lys Pro Asp Gly Phe Pro Thr Leu Leu Phe Phe Pro Ala Gly Asn  
           145                                  150                                  155                                  160  
 Lys Ser Phe Asp Pro Ile Thr Val Asp Thr Asp Arg Thr Val Val Ala  
                                   165                                  170                                  175  
 Phe Tyr Lys Phe Leu Lys Lys His Ala Ser Ile Pro Phe Lys Leu Gln  
                                   180                                  185                                  190  
 Lys Pro Thr Ser Thr Ser Glu Ser Asp Ser Lys Gly Ser Ser Asp Ala  
           195                                  200                                  205  
 Lys Glu Ser Gln Ser Ser Asp Val Lys Asp Glu Leu  
           210                                  215                                  220

<210> 13  
 <211> 1126  
 <212> DNA  
 <213> Glycine max

<400> 13  
 gcacgagcaa gtttccatta gttacaaagc tgactgaaat gaattctatc agagtctact 60  
 ccagcccat caagcttcag gtttagtct ttgcaaacat tgatgacttc aagaatcttc 120  
 ttgaaactct tcaagatgtt gcaaaaacat tcaagtcaaa gataatgttt atatatgtgg 180  
 atattaatga tgagaacctt gcaaagccct tcttaacatt gtttggctct gaagaatcaa 240  
 aaaatactgt ggtcgccgca ttgataatg caatgagctc aaaatatttg ttggagacaa 300  
 aaccaacaca aagcaatatt gaagagttct gcaataacct tgtgcaaggg tctttgtcac 360  
 cttacttcaa gtcacagcca attccagata atacagaatc aagtgtccat gttattgtcg 420  
 ggaaaacatt tgatgatgaa atcttgagca gcgagaagga tgtgctcttg gaggtattta 480  
 cgccttggtg catcaactgt gaggccacta gcaagcaagt agagaagttg gcaaagcact 540  
 acaaaggatc aagtaatcta atatttgcaa ggatagatgc ttcagcaaat gaacatccaa 600  
 aactgcaagt gaatgactac cccacgcttc tactttacag agcagacgat aaggcaaatc 660  
 cgatcaaact ttccacaaaa tctagtttga aagagttggc tgcattccatt aacaaatag 720  
 taaaagtcaa gaatcaagtc gtcaaagatg agttatagaa catatcaaaa agttttggga 780  
 gaaaaacact taaccatgaa gaaagtaaaa cattatggaa agaaacaaat attatgttgt 840  
 cttgcgtaag cattttctaa tttttattaa cttttccct gccattttat ggtggtccaa 900  
 atatgagtta gtctattatt atttgagtta gcttactgct aaattgcgaa agctagtcaa 960  
 attataacat gtaatgaact acagaacata cttgatacac caaacattgt accgatcaac 1020

actttccatt tgcattcat agaaacctgc aaatcacagg cttaaagttg atgcattgac 1080  
 acatatcaaa ctcaagcttt tataattcga aaaaaaaaaa aaaaaa 1126

<210> 14  
 <211> 251  
 <212> PRT  
 <213> Glycine max

<400> 14

Thr Ser Lys Phe Pro Leu Val Thr Lys Leu Thr Glu Met Asn Ser Ile  
 1 5 10 15

Arg Val Tyr Ser Ser Pro Ile Lys Leu Gln Val Leu Val Phe Ala Asn  
 20 25 30

Ile Asp Asp Phe Lys Asn Leu Leu Glu Thr Leu Gln Asp Val Ala Lys  
 35 40 45

Thr Phe Lys Ser Lys Ile Met Phe Ile Tyr Val Asp Ile Asn Asp Glu  
 50 55 60

Asn Leu Ala Lys Pro Phe Leu Thr Leu Phe Gly Leu Glu Glu Ser Lys  
 65 70 75 80

Asn Thr Val Val Ala Ala Phe Asp Asn Ala Met Ser Ser Lys Tyr Leu  
 85 90 95

Leu Glu Thr Lys Pro Thr Gln Ser Asn Ile Glu Glu Phe Cys Asn Asn  
 100 105 110

Leu Val Gln Gly Ser Leu Ser Pro Tyr Phe Lys Ser Gln Pro Ile Pro  
 115 120 125

Asp Asn Thr Glu Ser Ser Val His Val Ile Val Gly Lys Thr Phe Asp  
 130 135 140

Asp Glu Ile Leu Ser Ser Glu Lys Asp Val Leu Leu Glu Val Phe Thr  
 145 150 155 160

Pro Trp Cys Ile Asn Cys Glu Ala Thr Ser Lys Gln Val Glu Lys Leu  
 165 170 175

Ala Lys His Tyr Lys Gly Ser Ser Asn Leu Ile Phe Ala Arg Ile Asp  
 180 185 190

Ala Ser Ala Asn Glu His Pro Lys Leu Gln Val Asn Asp Tyr Pro Thr  
 195 200 205

Leu Leu Leu Tyr Arg Ala Asp Asp Lys Ala Asn Pro Ile Lys Leu Ser  
 210 215 220

Thr Lys Ser Ser Leu Lys Glu Leu Ala Ala Ser Ile Asn Lys Tyr Val  
 225 230 235 240

Lys Val Lys Asn Gln Val Val Lys Asp Glu Leu  
 245 250

<210> 15  
 <211> 1943  
 <212> DNA

<213> Glycine max

<400> 15

```
gttctcttca ctctcacaat gccaatcctc gttgtgctct ctctcgccac cctcctcctc 60
ttctcctccc tctttctcac cctctgcgac gacctcaccg acgacgagga cctcggcttc 120
ctcgacgagc cctccgccgc gccggagcac ggccactacc acgacgatga cgccaatttc 180
ggcgacttcg aggaggaccc ggaggcgtac aagcagcccg aggtggacga gaaggacgtc 240
gtcattttga aggagaagaa cttcaccgac accgtcaaga gcaaccgctt cgtcatgggtc 300
gagttctacg cgccctgggtg cggccactgc caggccctcg cgccggagta cgccgccgcc 360
gcgacggaac tcaaggcgca agacgtaatt ttggcaaagg tggatgccac cgaggagaat 420
gaattggcgc agcagtacga tgttcagggt ttccccactg tccacttctt cgttgatggc 480
attcacaagc cttataatgg ccaaaggacc aaagatgcta tagtgacgtg gataggaaag 540
aagatcggac ctggcatata caacttgact acagtggagg atgctcaacg catcttgacc 600
aacgaaacta aagttgtttt gggcttcctc aactctttag ttggtcctga gagtgaggag 660
cttgctgctg cttcaagact tgaggatgat gtcaattttt atcaaactgt ggatcctgat 720
gtggcaaagc ttttccatat tgaccagat gttaagcgcc cagctttgat cctcgtcaag 780
aaagaggagg aaaaacttaa ccactttgat ggcaaatttg agaagtcgga aatagcagac 840
tttgtcttct ccaacaagct tcctttggta acaattttta caagagaaaag tgccccatca 900
gtcttcgaaa atccaatcaa gaaacagttg ttgctgtttg caacttcaaa tgattcagag 960
aagttgatcc ctgcatttaa agaagctgca aaatctttca agggaaaagt gatctttgta 1020
tatgtggaaa tggataacga agatgttggg aagcctgttt cagaatactt tggatatcag 1080
gggaatgctc caaaagtact tgggtacact gggaatgatg atggaaaaaa atttgtgctt 1140
gatggagagg tgactgctga caaaattaag gcatttgggg acgatttcct tgaagacaag 1200
ctaaaacctt tttacaagtc agatccagtt cctgaaagta atgatggtga tgtgaaaata 1260
gtagttggga ataattttga tgaaattgtc ttggatgagt caaaggatgt tctcctcgag 1320
atztatgctc cttggtgtgg ccattgcca gcaactggagc caatatacga caagcttgca 1380
aaacatcttc gtaatatgga gtctcttgta atagccaaga tggatggaac aacaaatgag 1440
catcccaggg ctaagcctga tggatttccc actctcctct tcttcccggc aggaaacaag 1500
agttttgacc ctattactgt tgatacagat cgtacagtgg tagccttcta caagttcctc 1560
aagaaacatg catcaatccc attcaagctc cagaaaccaa cctcaacttc tgatgccaa 1620
gggagctctg atgccaaaga gagccagagt agtgatgtga aggatgaatt atgaggagtt 1680
aagtgatata tttttattta ttgaaactga ttcagacaga tgatgacatg gtgactgagg 1740
gagaaaatac caagctgctt ctctcccta gccaaataaaa acaaacgagg agtgggggga 1800
aggagacaaa tgcgaggcac atatgtatta ctattaactt aaatttttac aactgggcat 1860
tttagaattt tgggttgaga cttcaataaaa ttccccctta aatttttaaaa aaaaaaaaaa 1920
aaaaaaaaac tcgagactag ttc 1943
```

<210> 16

<211> 551

<212> PRT

<213> Glycine max

<400> 16

Met Arg Ile Leu Val Val Leu Ser Leu Ala Thr Leu Leu Leu Phe Ser  
1 5 10 15

Ser Leu Phe Leu Thr Leu Cys Asp Asp Leu Thr Asp Asp Glu Asp Leu  
20 25 30

Gly Phe Leu Asp Glu Pro Ser Ala Ala Pro Glu His Gly His Tyr His  
35 40 45

Asp Asp Asp Ala Asn Phe Gly Asp Phe Glu Glu Asp Pro Glu Ala Tyr  
50 55 60

Lys Gln Pro Glu Val Asp Glu Lys Asp Val Val Ile Leu Lys Glu Lys  
65 70 75 80

Asn Phe Thr Asp Thr Val Lys Ser Asn Arg Phe Val Met Val Glu Phe  
85 90 95

Tyr Ala Pro Trp Cys Gly His Cys Gln Ala Leu Ala Pro Glu Tyr Ala  
 100 105 110  
 Ala Ala Ala Thr Glu Leu Lys Gly Glu Asp Val Ile Leu Ala Lys Val  
 115 120 125  
 Asp Ala Thr Glu Glu Asn Glu Leu Ala Gln Gln Tyr Asp Val Gln Gly  
 130 135 140  
 Phe Pro Thr Val His Phe Phe Val Asp Gly Ile His Lys Pro Tyr Asn  
 145 150 155 160  
 Gly Gln Arg Thr Lys Asp Ala Ile Val Thr Trp Ile Gly Lys Lys Ile  
 165 170 175  
 Gly Pro Gly Ile Tyr Asn Leu Thr Thr Val Glu Asp Ala Gln Arg Ile  
 180 185 190  
 Leu Thr Asn Glu Thr Lys Val Val Leu Gly Phe Leu Asn Ser Leu Val  
 195 200 205  
 Gly Pro Glu Ser Glu Glu Leu Ala Ala Ala Ser Arg Leu Glu Asp Asp  
 210 215 220  
 Val Asn Phe Tyr Gln Thr Val Asp Pro Asp Val Ala Lys Leu Phe His  
 225 230 235 240  
 Ile Asp Pro Asp Val Lys Arg Pro Ala Leu Ile Leu Val Lys Lys Glu  
 245 250 255  
 Glu Glu Lys Leu Asn His Phe Asp Gly Lys Phe Glu Lys Ser Glu Ile  
 260 265 270  
 Ala Asp Phe Val Phe Ser Asn Lys Leu Pro Leu Val Thr Ile Phe Thr  
 275 280 285  
 Arg Glu Ser Ala Pro Ser Val Phe Glu Asn Pro Ile Lys Lys Gln Leu  
 290 295 300  
 Leu Leu Phe Ala Thr Ser Asn Asp Ser Glu Lys Leu Ile Pro Ala Phe  
 305 310 315 320  
 Lys Glu Ala Ala Lys Ser Phe Lys Gly Lys Leu Ile Phe Val Tyr Val  
 325 330 335  
 Glu Met Asp Asn Glu Asp Val Gly Lys Pro Val Ser Glu Tyr Phe Gly  
 340 345 350  
 Ile Ser Gly Asn Ala Pro Lys Val Leu Gly Tyr Thr Gly Asn Asp Asp  
 355 360 365  
 Gly Lys Lys Phe Val Leu Asp Gly Glu Val Thr Ala Asp Lys Ile Lys  
 370 375 380  
 Ala Phe Gly Asp Asp Phe Leu Glu Asp Lys Leu Lys Pro Phe Tyr Lys  
 385 390 395 400  
 Ser Asp Pro Val Pro Glu Ser Asn Asp Gly Asp Val Lys Ile Val Val  
 405 410 415

Gly Asn Asn Phe Asp Glu Ile Val Leu Asp Glu Ser Lys Asp Val Leu  
 420 425 430

Leu Glu Ile Tyr Ala Pro Trp Cys Gly His Cys Gln Ala Leu Glu Pro  
 435 440 445

Ile Tyr Asp Lys Leu Ala Lys His Leu Arg Asn Ile Glu Ser Leu Val  
 450 455 460

Ile Ala Lys Met Asp Gly Thr Thr Asn Glu His Pro Arg Ala Lys Pro  
 465 470 475 480

Asp Gly Phe Pro Thr Leu Leu Phe Phe Pro Ala Gly Asn Lys Ser Phe  
 485 490 495

Asp Pro Ile Thr Val Asp Thr Asp Arg Thr Val Val Ala Phe Tyr Lys  
 500 505 510

Phe Leu Lys Lys His Ala Ser Ile Pro Phe Lys Leu Gln Lys Pro Thr  
 515 520 525

Ser Thr Ser Asp Ala Lys Gly Ser Ser Asp Ala Lys Glu Ser Gln Ser  
 530 535 540

Ser Asp Val Lys Asp Glu Leu  
 545 550

<210> 17  
 <211> 1565  
 <212> DNA  
 <213> Triticum aestivum

<400> 17  
 gcacgagacc acgcggagct gctgctgctc ggggtacgcgc cgtgggtgtga gcgcagcgcgc 60  
 cagctcatgc cgcggttcgc cgaggccgcc gccgcgctgc gcgccatggg cagcgcgcgc 120  
 gccttcgcga agctcgacgg ggagcgctac cccaaggcgg ctgccgccgt cgggggtcaag 180  
 ggcttcccca ccgtgctcct ctctcgtaac ggcaccgagc acgcctacca tggcctccac 240  
 accaaggacg ccatagttac ttgggtaaga aagaaaactg gcgagccaat cattaggctt 300  
 cagtctaagg attcagctga ggagttcctc aaaaaggaca tgacctttgt tattgggcta 360  
 ttcaagaatt ttgagggagc agaccatgaa gaatttgtga aggcagcaac cacagacaac 420  
 gagggtacagt ttgtagaaac cagtataaca cgtgttgcca aagttctatt tccagggtatt 480  
 acgtccgagg agaaatttgc gggcctcggt aaaagcgagc cagagaagtt tgaaaagttc 540  
 gatgggaaat ttgaagaaac ggaaattctg cggtttgtgg agctcaacaa gtttcctcta 600  
 attactgtat tcaactgagc caattccggt aaagtatatt caagccctat taagctacag 660  
 gtcttcacct ttgcagaggg ttatgatttt gaagatctgg aatctatggg tgaagaaata 720  
 gccagagcat tcaagacaaa gataatgttt atatatgttg aactgctga agaaaacctt 780  
 gcaaaacctat tctcactctt ttatggcctt gaatcagaaa aaaagcctac tgttacagca 840  
 tttgatacaa gcaatggagc caagtatctg atggaggcag atatcaatgc aaacaacctg 900  
 agggagttct gcttaagtct tctggatggc acgctcccgc cataccacaa atcagaacca 960  
 ttgcctcaag agaagggact tattgaaaag gttgttggtc gtacatttga ttcttctgtg 1020  
 ctggaaagtc atcaaaacgt ctcccttgag gttcatacac cttgggtgtg tgactgtgaa 1080  
 gcgataagta aaaatgttga gaagttggcg aagcatttca gtggttcgga caatcttaaa 1140  
 tttgcacgca tagatgcttc tgtgaatgaa catcccaaat tgaagtgaa taattccccg 1200  
 acgtatttcc tttatcttgc tgaagacaaa aacaaccgca tcaagctttc aaagaaatcg 1260  
 agtgtcaagg acatggccaa actgatcaag gagaagctgc aaataccaga cgtggagaca 1320  
 gtagcggccc ctgacaacgt caaggatgag ctataacctg tagtagacaa actaagggtcc 1380  
 agtgaaggaa aaattgcagc atgtttgcgt gttttgcccc aacctgatca cagagctcag 1440  
 ctttattcgc gtgctgtgtt aagttgacta aagtcattgg tatataatat aggtaccta 1500  
 atcaagaggc cttcggcccc taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1560

aaaaa

1565

<210> 18  
 <211> 451  
 <212> PRT  
 <213> Triticum aestivum

<400> 18  
 Ala Arg Asp His Ala Glu Leu Leu Leu Leu Gly Tyr Ala Pro Trp Cys  
 1 5 10 15  
 Glu Arg Ser Ala Gln Leu Met Pro Arg Phe Ala Glu Ala Ala Ala Ala  
 20 25 30  
 Leu Arg Ala Met Gly Ser Ala Val Ala Phe Ala Lys Leu Asp Gly Glu  
 35 40 45  
 Arg Tyr Pro Lys Ala Ala Ala Ala Val Gly Val Lys Gly Phe Pro Thr  
 50 55 60  
 Val Leu Leu Phe Val Asn Gly Thr Glu His Ala Tyr His Gly Leu His  
 65 70 75 80  
 Thr Lys Asp Ala Ile Val Thr Trp Val Arg Lys Lys Thr Gly Glu Pro  
 85 90 95  
 Ile Ile Arg Leu Gln Ser Lys Asp Ser Ala Glu Glu Phe Leu Lys Lys  
 100 105 110  
 Asp Met Thr Phe Val Ile Gly Leu Phe Lys Asn Phe Glu Gly Ala Asp  
 115 120 125  
 His Glu Glu Phe Val Lys Ala Ala Thr Thr Asp Asn Glu Val Gln Phe  
 130 135 140  
 Val Glu Thr Ser Asp Thr Arg Val Ala Lys Val Leu Phe Pro Gly Ile  
 145 150 155 160  
 Thr Ser Glu Glu Lys Phe Val Gly Leu Val Lys Ser Glu Pro Glu Lys  
 165 170 175  
 Phe Glu Lys Phe Asp Gly Lys Phe Glu Glu Thr Glu Ile Leu Arg Phe  
 180 185 190  
 Val Glu Leu Asn Lys Phe Pro Leu Ile Thr Val Phe Thr Glu Leu Asn  
 195 200 205  
 Ser Gly Lys Val Tyr Ser Ser Pro Ile Lys Leu Gln Val Phe Thr Phe  
 210 215 220  
 Ala Glu Ala Tyr Asp Phe Glu Asp Leu Glu Ser Met Val Glu Glu Ile  
 225 230 235 240  
 Ala Arg Ala Phe Lys Thr Lys Ile Met Phe Ile Tyr Val Asp Thr Ala  
 245 250 255  
 Glu Glu Asn Leu Ala Lys Pro Phe Leu Thr Leu Tyr Gly Leu Glu Ser  
 260 265 270  
 Glu Lys Lys Pro Thr Val Thr Ala Phe Asp Thr Ser Asn Gly Ala Lys



275                      280                      285  
 Tyr Leu Met Glu Ala Asp Ile Asn Ala Asn Asn Leu Arg Glu Phe Cys  
 290                      295                      300  
 Leu Ser Leu Leu Asp Gly Thr Leu Pro Pro Tyr His Lys Ser Glu Pro  
 305                      310                      315                      320  
 Leu Pro Gln Glu Lys Gly Leu Ile Glu Lys Val Val Gly Arg Thr Phe  
 325                      330                      335  
 Asp Ser Ser Val Leu Glu Ser His Gln Asn Val Phe Leu Glu Val His  
 340                      345                      350  
 Thr Pro Trp Cys Val Asp Cys Glu Ala Ile Ser Lys Asn Val Glu Lys  
 355                      360                      365  
 Leu Ala Lys His Phe Ser Gly Ser Asp Asn Leu Lys Phe Ala Arg Ile  
 370                      375                      380  
 Asp Ala Ser Val Asn Glu His Pro Lys Leu Lys Val Asn Asn Ser Pro  
 385                      390                      395                      400  
 Thr Leu Phe Leu Tyr Leu Ala Glu Asp Lys Asn Asn Pro Ile Lys Leu  
 405                      410                      415  
 Ser Lys Lys Ser Ser Val Lys Asp Met Ala Lys Leu Ile Lys Glu Lys  
 420                      425                      430  
 Leu Gln Ile Pro Asp Val Glu Thr Val Ala Ala Pro Asp Asn Val Lys  
 435                      440                      445  
 Asp Glu Leu  
 450

<210> 19  
 <211> 1078  
 <212> DNA  
 <213> Triticum aestivum

<400> 19  
 gcacgaggtt cagagcatct gcgattgcca agtttgtttc ggccaacaaa atcccattga 60  
 tcaccaccct cacacaggag accgcccctg cgatttttga taatccgata aagaagcaaa 120  
 ttttgctgtt tgctgttgcg aaggagtctt caaaatttct gccatcatt aaggaaacag 180  
 caaaatcatt caaggggaag cttttatttg tctttgtgga gcgtgacaat gaggaagttg 240  
 gcgaacctgt tgccaattac tttggaatta ctggacaaga gaccacggtt cttgcttaca 300  
 ctgggaatga agacgctaag aagttcttct tcaccggtga aatatcactg gacaccatta 360  
 aggaatttgc tcaagatttc atggaggaca agctcacacc atctacaag tctgaccag 420  
 tacctgaatc caatgatgag gacgtcaaag ttgttggttg caagagtcta gatcaaatag 480  
 ttctggatga gtcaaaggat gtcttttttg agatatatgc gccatggtgt ggccattgtc 540  
 agtcactgga gcctatctac aacaagctgg ccaagtacct ccgtggcatt gactcccttg 600  
 taatagccaa aatggacggc acaaacaatg agcatcctcg tgccaagccc gatgggttcc 660  
 ccacgatact cttctacca gctgggaaga aaagctttga gcctataact ttcgaggggg 720  
 gccggacagt ggtagagatg tacaagttcc tcaagaagca tgccgccatc cttttcaagc 780  
 tcaagcgccc ggactcgtca gcggcacgga ccgacagcgc cgagggccca ggctcgacca 840  
 ccgacagcga gaagagctcc ggctcgaacc cgaaggacga gttgtagggg attgacaagt 900  
 acgaggaggc gccgatgatg tcgaaatcag gaggtggaga aggaatggct aagctaggta 960  
 tcaaccaacc ttggctgctg caagtgtatg ctgacaacac aaatattaac tgctgtagaa 1020  
 tccaataaaa taaaagcaag aggtcctttt tcttagtact aaaaaaaaaa aaaaaaaaaa 1078

<210> 20  
 <211> 294  
 <212> PRT  
 <213> Triticum aestivum

<400> 20  
 Thr Arg Phe Arg Ala Ser Ala Ile Ala Lys Phe Val Ser Ala Asn Lys  
 1 5 10 15  
 Ile Pro Leu Ile Thr Thr Leu Thr Gln Glu Thr Ala Pro Ala Ile Phe  
 20 25 30  
 Asp Asn Pro Ile Lys Lys Gln Ile Leu Leu Phe Ala Val Ala Lys Glu  
 35 40 45  
 Ser Ser Lys Phe Leu Pro Ile Ile Lys Glu Thr Ala Lys Ser Phe Lys  
 50 55 60  
 Gly Lys Leu Leu Phe Val Phe Val Glu Arg Asp Asn Glu Glu Val Gly  
 65 70 75 80  
 Glu Pro Val Ala Asn Tyr Phe Gly Ile Thr Gly Gln Glu Thr Thr Val  
 85 90 95  
 Leu Ala Tyr Thr Gly Asn Glu Asp Ala Lys Lys Phe Phe Phe Thr Gly  
 100 105 110  
 Glu Ile Ser Leu Asp Thr Ile Lys Glu Phe Ala Gln Asp Phe Met Glu  
 115 120 125  
 Asp Lys Leu Thr Pro Ser Tyr Lys Ser Asp Pro Val Pro Glu Ser Asn  
 130 135 140  
 Asp Glu Asp Val Lys Val Val Val Gly Lys Ser Leu Asp Gln Ile Val  
 145 150 155 160  
 Leu Asp Glu Ser Lys Asp Val Leu Leu Glu Ile Tyr Ala Pro Trp Cys  
 165 170 175  
 Gly His Cys Gln Ser Leu Glu Pro Ile Tyr Asn Lys Leu Ala Lys Tyr  
 180 185 190  
 Leu Arg Gly Ile Asp Ser Leu Val Ile Ala Lys Met Asp Gly Thr Asn  
 195 200 205  
 Asn Glu His Pro Arg Ala Lys Pro Asp Gly Phe Pro Thr Ile Leu Phe  
 210 215 220  
 Tyr Pro Ala Gly Lys Lys Ser Phe Glu Pro Ile Thr Phe Glu Gly Gly  
 225 230 235 240  
 Arg Thr Val Val Glu Met Tyr Lys Phe Leu Lys Lys His Ala Ala Ile  
 245 250 255  
 Pro Phe Lys Leu Lys Arg Pro Asp Ser Ser Ala Ala Arg Thr Asp Ser  
 260 265 270  
 Ala Glu Gly Pro Gly Ser Thr Thr Asp Ser Glu Lys Ser Ser Gly Ser  
 275 280 285

Asn Pro Lys Asp Glu Leu  
290